In the Claims

1. (Currently Amended) ~~Method~~ A method for producing a protein, the method comprising the steps of:

(a) providing a nucleic acid sequence coding for the protein wherein the nucleic acid sequence coding for the protein comprises a translation start codon;

(b) inserting ~~in which~~ a heterologous nucleic acid sequence ~~is inserted~~ on the 3' side of the translation start codon in the correct reading frame, wherein said heterologous nucleic acid sequence ~~being selected such that~~ forms a stem-loop structure ~~is formed~~ on the 3' side of the translation start codon ~~at a distance of~~ 6-30 nucleotides from the 3' side of the start codon~~,~~;

(~~b~~c) providing an expression system ~~suitable~~ for ~~expressing~~ the protein; ~~and~~

(~~c~~d) introducing the nucleic acid ~~sequence~~ sequences combined in step (b)~~according to (a)~~ into the expression system; and

(e) ~~according to (b) under conditions such that a~~ forming the stem-loop structure ~~is formed~~ wherein the length of the stem is in the range of 4-12 nucleotides.

2. (Currently Amended) ~~Method~~ The method as claimed in claim 1 ~~additionally~~ further comprising ~~the isolation of~~ the step of isolating the protein.

3. (Currently Amended) ~~Method~~ The method as claimed in claim 1 ~~or 2, characterized in that,~~ wherein the ~~inserted~~ heterologous nucleic acid sequence has a length of up to 201 nucleotides.

4. (Currently Amended) ~~Method~~ The method as claimed in claim 3~~,~~ ~~characterized in that~~ wherein the ~~inserted~~ heterologous nucleic acid sequence has a length of up to 45 nucleotides.

5. (Currently Amended) ~~Method~~ The method as claimed in ~~one of the claims 1 to 4, characterized in that~~ claim 1 wherein the stem-loop structure is formed ~~at a distance of~~ 12-21 nucleotides ~~on~~ from the 3' side of the start codon.

6. (Currently Amended) ~~Method~~ The method as claimed in ~~one of the claims 1 to 5, characterized in that~~ claim 1 wherein the region of the heterologous nucleic acid

sequence that is on the 5' side of the stem-loop structure does not ~~itself~~ form a secondary structure ~~and cannot form a secondary structure~~ with the 5' untranslated region of the nucleic acid sequence coding for the protein ~~to be produced~~.

7. (Currently Amended) ~~Method~~ The method as claimed in ~~one of the claims 1 to 6, characterized in that~~ claim 1 wherein the region of the heterologous nucleic acid sequence that is on the 5' side of the stem-loop structure and on the 3' side of the ~~ATG~~ start codon has a GC content of ~~<~~ less than 50 %.

8. (Currently Amended) ~~Method~~ The method as claimed in ~~one of the claims 1 to 7, characterized in that~~ claim 1 wherein an *in vitro* expression system is used.

9. (Currently Amended) ~~Method~~ The method as claimed in ~~one of the claims 1 to 8, characterized in that~~ claim 8 wherein ~~a prokaryotic~~the *in vitro* expression system is a prokaryotic *in vitro* expression system ~~used~~.

10. (Currently Amended) ~~Method~~ The method as claimed in claim 9~~,~~ ~~characterized in that~~ wherein the prokaryotic *in vitro* expression system comprises a lysate~~lysates~~ of ~~gram-negative bacteria, in particular of~~ *Escherichia coli* ~~of gram-positive bacteria, in particular of~~ or of *Bacillus subtilis*.

11. (Currently Amended) ~~Method~~ The method as claimed in claim 8~~,~~ ~~characterized in that~~ wherein ~~a eukaryotic~~ the *in vitro* expression system is a eukaryotic *in vitro* expression system ~~used~~.

12. (Currently Amended) ~~Method~~ The method as claimed in claim 11~~,~~ ~~characterized in that~~ wherein the eukaryotic *in vitro* expression system comprises a lysate selected from the group consisting of a lysate ~~lysates~~ of mammalian cells ~~in particular of rabbits~~, reticulocytes, human tumour cell lines, hamster cell lines~~,~~ ~~or~~ other vertebrate cells~~,~~ ~~in particular~~ oocytes~~,~~ ~~and~~ eggs of fish, eggs of ~~and~~ amphibia~~,~~ ~~as well as~~ insect cell lines, yeast cells, algal cells~~,~~ ~~or~~ and extracts of plant seedlings.

13. (Currently Amended) ~~Method~~ The method as claimed in ~~one of the claims 1 to 7, characterized in that~~ claim 1 wherein the expression system is a prokaryotic *in vivo* expression system ~~is used~~.

14. (Cancelled)

15. (Currently Amended) ~~Method~~ The method as claimed in claim 13~~14,~~ ~~characterized in that~~ wherein the ~~a gram-negative~~ prokaryotic expression system~~host cell, in particular~~ comprises an *E. coli* cell or a ~~gram-positive prokaryotic host cell, in particular a~~ *Bacillus subtilis* cell ~~is used~~.

16. (Currently Amended) ~~Method~~ The method as claimed in ~~one of the claims 1 to 7, characterized in that~~ claim 1 wherein the expression system comprises a eukaryotic host cell ~~is used as an expression system~~.

17. (Currently Amended) ~~Method~~ The method as claimed in claim 16~~,~~ ~~characterized in that~~ wherein the eukaryotic host cell is selected from the group consisting of a yeast cell, an insect cell, ~~or a vertebrate cell, in particular~~ an amphibian cell, a fish cell, a bird cell, ~~and~~ a ~~or~~ mammalian cell, and a vertebrate cell ~~is used~~.

18. (Currently Amended) ~~Method~~ The method as claimed in ~~one of the claims 1 to 7, characterized in that~~ claim 16 wherein the expression system is a non-human eukaryotic host organism ~~is used as the expression system~~.

19. (Currently Amended) ~~Method~~ The method as claimed in ~~one of the claims 1 to 18, characterized in that~~ claim 1 wherein the nucleic acid sequence coding for the protein is provided by a method selected from the group consisting of cloning, recombination ~~or~~/and amplification.

20. (Currently Amended) ~~Method~~ The method as claimed in claim 19~~,~~ ~~characterized in that~~ wherein the nucleic acid sequence coding for the protein is provided by ~~provision comprises~~ a two-step ~~PCR~~polymerase chain reaction.

21. (Currently Amended) ~~Method~~ The method as claimed in ~~one of the claims 1 to 20, characterized in that~~ claim 1 wherein the nucleic acid sequence coding for the protein ~~to be produced~~ or/~~and~~ the heterologous nucleic acid sequence comprises ~~at least partially have~~ a codon ~~usage~~ adapted, based on codon usage, to the ~~respective~~ expression system.

22. (Currently Amended) ~~Method~~ The method as claimed in ~~one of the claims 1 to 21, characterized in that~~ claim 1 wherein the heterologous nucleic acid sequence comprises ~~contains a section~~ coding sequence for a purification domain or/~~and a section coding~~ for a proteinase recognition domain.

23. (Currently Amended) ~~Reagent~~ A composition for producing a protein, the composition comprising:

(a) a nucleic acid sequence that is heterologous to the nucleic acid sequence coding for the protein ~~which can be~~ wherein the heterologous nucleic acid sequence is inserted into the protein-coding nucleic acid sequence in the correct reading frame and wherein the heterologous nucleic acid sequence ~~which can form~~ forms a stem-loop structure ~~at a distance of~~ 6-30 nucleotides ~~on~~ from the 3' side of the translation start codon~~,~~; and

(b) an expression system ~~that is suitable~~ for ~~producing~~ the protein.